

M. Pak

#17
P. P. P.

1646

RAW SEQUENCE LISTING DATE: 08/09/2000
 PATENT APPLICATION: US/09/072,994A TIME: 13:57:35

Input Set : A:\Miv03202.app
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SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Cottarel, Guillaume
 7 Damagnez, Veronique
 8 Draetta, Guilo
 10 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
 11 Human Pathogens, and Uses Related Thereto
 13 (iii) NUMBER OF SEQUENCES: 27
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 17 (B) STREET: One Post Office Square
 18 (C) CITY: Boston
 19 (D) STATE: MA
 20 (E) COUNTRY: USA
 21 (F) ZIP: 02109-2170
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/072,994A
 C--> 31 (B) FILING DATE: 05-May-1998
 32 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: US 08/463,090
 36 (B) FILING DATE: 05-JUN-1995
 38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Vincent, Matthew P.
 40 (B) REGISTRATION NUMBER: 36,709
 41 (C) REFERENCE/DOCKET NUMBER: MIV-032.02
 43 (ix) TELECOMMUNICATION INFORMATION:
 44 (A) TELEPHONE: 617-832-1000
 45 (B) TELEFAX: 617-832-7000
 48 (2) INFORMATION FOR SEQ ID NO: 1:
 50 (i) SEQUENCE CHARACTERISTICS:
 51 (A) LENGTH: 1668 base pairs
 52 (B) TYPE: nucleic acid
 53 (C) STRANDEDNESS: both
 54 (D) TOPOLOGY: linear
 56 (ii) MOLECULE TYPE: cDNA
 59 (ix) FEATURE:
 60 (A) NAME/KEY: CDS
 61 (B) LOCATION: 259..1491
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 66 GGATGATACA AATGTGGAAG ATGCAAATTG TTCTCCCTT ACTTTGATGA GAAAAAGTGC 60
 68 ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAATAATT CCAATCACC ATCGCCAAC 120

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72 AGAAATTAT CTAATTTCGT TATTCCTTCG TCAGTTAAAT CAAAAACGAA ACAATTTACA 240
74 AACTCTTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA 291
75           Met Thr Glu Val Val Ser Lys Ser Ser His Ser
76           1           5           10
78 TTT TTC AAT AAT TTG CAT CTT GCA ACC TCA ACT GCG TCT TCT TCA GTA 339
79 Phe Phe Asn Asn Leu His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val
80           15           20           25
82 TCG AGC ACA ACT CCC AAA ATA GAA TTC AAT TCC ATA GCT GAA AAT GAT 387
83 Ser Ser Thr Thr Pro Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp
84           30           35           40
86 GAT ATC CCT ACC AAT TAT GAC TCT GAT GAA GAA TTC GAA GAT GGT GAT 435
87 Asp Ile Pro Thr Asn Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp
88           45           50           55
90 ACG TTT ATA CAA TCC ACC TTG ATT CAC CAG TTC AAC GCA AGT CAA GTA 483
91 Thr Phe Ile Gln Ser Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val
92 60           65           70           75
94 ACA ACA ACA ACA ATA ATA ATA CCA ATG ATG GTA ACG ACA ATA ATA 531
95 Thr Thr Thr Thr Ile Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile
96           80           85           90
98 TAC CTA CAA AAA TTA GAC GGT TCC ACT CCA TGT ACC AAA CCG ATA AAG 579
99 Tyr Leu Gln Lys Leu Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys
100           95           100           105
102 AGA TTG CAT CGT ACC AAC TTC ATG AAG ATA ATT CAT TTT GAA ATT TAC 627
103 Arg Leu His Arg Thr Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr
104           110           115           120
106 AAT ATT GAA TAT TCT CAT CTG GAG AGT GAT TTG TTA CCA CGA ATC GAT 675
107 Asn Ile Glu Tyr Ser His Leu Glu Ser Asp Leu Leu Pro Arg Ile Asp
108           125           130           135
110 GCT CAT CAA TTA GCC AGA ATA TTA CGT GGA GAC CAC GAT GAC CAA TTT 723
111 Ala His Gln Leu Ala Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe
112 140           145           150           155
114 GAT GAA TTT ATT ATC ATT GAT TGT CGA TTT GAG TAT GAA TTT AAT GGT 771
115 Asp Glu Phe Ile Ile Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly
116           160           165           170
118 GGC CAT ATT ACT AGG GCA ATC AAT ATC TCC ACC CAG GAA GCA CTT CAA 819
119 Gly His Ile Thr Arg Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln
120           175           180           185
122 GAA AAG CTC TTT CAA TAT CAA GAA ACA GAT ACC AAG GAC ACT GAA AGC 867
123 Glu Lys Leu Phe Gln Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser
124           190           195           200
126 AAG AAG CGA TTG ATA ATT TTC CAT TGT GAG TTC AGT ATG TTC AGA GGA 915
127 Lys Lys Arg Leu Ile Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly
128           205           210           215
130 CCA ATG ATG GCC AAA CAT TTA AGA AAG TGT GAT AGA ATG TGC AAC TAC 963
131 Pro Met Met Ala Lys His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr
132 220           225           230           235
134 GAC AAT TAT CCT CTA TTA ACA TAC CCC GAT ATT GCA ATT TTG GAA GGA 1011
135 Asp Asn Tyr Pro Leu Leu Thr Tyr Pro Asp Ile Ala Ile Leu Glu Gly

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139 Gly Tyr Lys Asn Phe Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln
140          255          260          265
142 GGA TAT GTC GAG ATG AAG AAT TTA CGA CAC AAA AAA TTA TGT GAA TCC 1107
143 Gly Tyr Val Glu Met Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser
144          270          275          280
146 AAC TTG GAT AAA GTT AGA AAA GAT AAT AAA CTA ACT AGA GCA AAG TCT 1155
147 Asn Leu Asp Lys Val Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser
148          285          290          295
150 TAT CAA TTT GGT ATT CAA CAC CGC CGT GGT GGT TCC ACT GGT GGA CTT 1203
151 Tyr Gln Phe Gly Ile Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu
152 300          305          310          315
154 TTC GGC AAC TAT AAT TAC AAC GTT ATG AAC TCA TCA GAT CAA CAA TTT 1251
155 Phe Gly Asn Tyr Asn Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe
156          320          325          330
158 TGG AGT AGC AGT ACT TCC AAC ACT GCT CAC CAC AGA AGT AGT AGC AGT 1299
159 Trp Ser Ser Ser Thr Ser Asn Thr Ala His His Arg Ser Ser Ser Ser
160          335          340          345
162 AGC GGG TTC ATT AAT AAT ATG CAT AGT GGT GCT TCG TCA TAT CAC CAT 1347
163 Ser Gly Phe Ile Asn Asn Met His Ser Gly Ala Ser Ser Tyr His His
164          350          355          360
166 AGG TCA CAA TCG TTT GTA ACT ATC AAT AAT GAG AAA ATT ATC AAG CGA 1395
167 Arg Ser Gln Ser Phe Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg
168          365          370          375
170 CAA AGA TCG ACT CCC AAA GTC AGC AAC TCA CCA ACC AAG CCA CCT CAT 1443
171 Gln Arg Ser Thr Pro Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His
172 380          385          390          395
174 CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT 1491
175 Gln Leu Tyr Leu Leu Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp
176          400          405          410
178 TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT 1551
180 CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT 1611
182 CTGAATTATC AGTCAATACT CAAGATTTTC AACCACCGAC TACGTCCTTT AGGAATT 1668
186 (2) INFORMATION FOR SEQ ID NO: 2:
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 786 base pairs
190 (B) TYPE: nucleic acid
191 (C) STRANDEDNESS: both
192 (D) TOPOLOGY: linear
194 (ii) MOLECULE TYPE: cDNA
197 (ix) FEATURE:
198 (A) NAME/KEY: CDS
199 (B) LOCATION: 208..513
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
204 AACTTGTTTA CTTATTGTT TATATAATTG ATAGATATCA ATTACTAATT TACCCTTGTT 60
206 TTTTACTTCC TACTATTCAA GACTTTATTT CCTCCTGATA ATCATTTTGT TTGATTATCA 120
208 TTTTCGTCAA TTAGTTCTTT TTTTTCATTT GTTCCAGAG TTTAGGAAGA CTACATTTT 180
210 ACAATTTTCA ATTCAAATAT TTTCCCA ATG ACT AAA CCA AGA TTT TTA ACA 231

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211           .           Met Thr Lys Pro Arg Phe Leu Thr
212           1           5
214 AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC      279
215 Arg Tyr Arg Lys Ser Lys Ser Val Gly Ile Ser Asp Met Ile His Tyr
216   10           15           20
218 AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA      327
219 Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu
220  25           30           35           40
222 CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA      375
223 Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu
224           45           50           55
226 ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA GAA TGG AGA GGG TTA GGA      423
227 Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly
228           60           65           70
230 ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG      471
231 Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu
232           75           80           85
234 CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA      513
235 Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln
236   90           95           100
238 TAAAAAGATT AACTATATTT GAATACTATA GAATCGGAAT CGGTTTAAAA GTTAACACTG      573
240 GAATTAAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA      633
242 CCCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTTGTATA CACTATTTAT      693
244 AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA      753
246 AACTGTATAA ATACTCTTGG TACCTCGCAT GTT      786
250 (2) INFORMATION FOR SEQ ID NO: 3:
252   (i) SEQUENCE CHARACTERISTICS:
253       (A) LENGTH: 1002 base pairs
254       (B) TYPE: nucleic acid
255       (C) STRANDEDNESS: both
256       (D) TOPOLOGY: linear
258   (ii) MOLECULE TYPE: cDNA
261   (ix) FEATURE:
262       (A) NAME/KEY: CDS
263       (B) LOCATION: 43..993
266   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
268 TAGAACACAC ACATCCCAAG CCAAGACCAA CACTTATTGC AA ATG GTA GAG TTA      54
269           Met Val Glu Leu
270           1
272 TCT GAT TAT CAA CGT CAA GAA AAA GTC GGA GAA GGT ACT TAT GGG GTT      102
273 Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly Thr Tyr Gly Val
274   5           10           15           20
276 GTT TAT AAA GCA TTA GAT ACC AAG CAC AAT AAT AGA GTT GTT GCA TTA      150
277 Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg Val Val Ala Leu
278           25           30           35
280 AAG AAA ATT CGA TTA GAA TCA GAA GAT GAA GGT GTA CCT AGT ACC GCC      198
281 Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val Pro Ser Thr Ala
282           40           45           50
284 ATT AGA GAA ATC TCG TTA TTA AAA GAA ATG AAA GAT GAT AAT ATC GTT      246

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288	CGA	TTA	TAT	GAT	ATT	ATT	CAT	TCA	GAT	TCT	CAT	AAA	TTA	TAT	TTA	GTA	294
289	Arg	Leu	Tyr	Asp	Ile	Ile	His	Ser	Asp	Ser	His	Lys	Leu	Tyr	Leu	Val	
290		70					75					80					
292	TTT	GAA	TTT	TTG	GAT	TTA	GAT	TTA	AAG	AAA	TAT	ATG	GAA	AGT	ATT	CCT	342
293	Phe	Glu	Phe	Leu	Asp	Leu	Asp	Leu	Lys	Lys	Tyr	Met	Glu	Ser	Ile	Pro	
294		85					90				95					100	
296	CAA	GGA	GTT	GGA	CTA	GGG	GCT	AAT	ATG	ATA	AAA	AGA	TTT	ATG	AAT	CAA	390
297	Gln	Gly	Val	Gly	Leu	Gly	Ala	Asn	Met	Ile	Lys	Arg	Phe	Met	Asn	Gln	
298				105						110					115		
300	TTA	ATT	CGA	GGT	ATT	AAA	CAT	TGT	CAT	TCT	CAT	CGA	GTT	TTA	CAT	CGT	438
301	Leu	Ile	Arg	Gly	Ile	Lys	His	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	
302				120						125				130			
304	GAT	TTA	AAA	CCA	CAA	AAT	TTA	TTG	ATT	GAT	AAA	GAA	GGG	AAT	TTA	AAA	486
305	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asp	Lys	Glu	Gly	Asn	Leu	Lys	
306			135					140					145				
308	TTA	GCA	GAT	TTT	GGA	TTA	GCT	CGA	GCA	TTT	GGA	GTT	CCA	TTA	AGA	GCA	534
309	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Leu	Arg	Ala	
310		150					155					160					
312	TAT	ACT	CAT	GAA	GTT	GTC	ACT	TTA	TGG	TAT	CGA	GCT	CCC	GAA	ATC	TTG	582
313	Tyr	Thr	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	
314	165					170				175					180		
316	TTA	GGA	GGG	AAA	CAA	TAT	TCC	ACT	GGG	GTA	GAT	ATG	TGG	TCT	GTT	GGA	630
317	Leu	Gly	Gly	Lys	Gln	Tyr	Ser	Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	
318				185						190				195			
320	TGT	ATA	TTT	GCT	GAA	ATG	TGT	AAT	AGG	AAA	CCA	TTA	TTT	CCT	GGT	GAT	678
321	Cys	Ile	Phe	Ala	Glu	Met	Cys	Asn	Arg	Lys	Pro	Leu	Phe	Pro	Gly	Asp	
322			200						205				210				
324	TCA	GAA	ATT	GAT	GAA	ATT	TTC	CGA	ATT	TTC	CGA	ATT	TTA	GGA	ACA	CCT	726
325	Ser	Glu	Ile	Asp	Glu	Ile	Phe	Arg	Ile	Phe	Arg	Ile	Leu	Gly	Thr	Pro	
326			215					220					225				
328	AAT	GAA	GAA	ATT	TGG	CCT	GAT	GTT	AAT	TAT	TTA	CCA	GAT	TTT	AAA	TCA	774
329	Asn	Glu	Glu	Ile	Trp	Pro	Asp	Val	Asn	Tyr	Leu	Pro	Asp	Phe	Lys	Ser	
330		230					235					240					
332	AGT	TTC	CCT	CAA	TGG	AAA	AAG	AAA	CCT	TTG	AGT	GAA	GCA	GTT	CCA	AGT	822
333	Ser	Phe	Pro	Gln	Trp	Lys	Lys	Lys	Pro	Leu	Ser	Glu	Ala	Val	Pro	Ser	
334	245					250					255				260		
336	TTG	GAT	GCT	AAT	GGA	ATT	GAT	CTT	TTG	GAT	CAA	ATG	TTG	GTG	TAT	GAT	870
337	Leu	Asp	Ala	Asn	Gly	Ile	Asp	Leu	Leu	Asp	Gln	Met	Leu	Val	Tyr	Asp	
338				265						270				275			
340	CCA	AGT	AGA	AGA	ATA	AGT	GCT	AAA	CGA	GCT	TTA	ATT	CAT	CCT	TAT	TTT	918
341	Pro	Ser	Arg	Arg	Ile	Ser	Ala	Lys	Arg	Ala	Leu	Ile	His	Pro	Tyr	Phe	
342			280						285					290			
344	AAT	GAT	AAT	GAT	CGT	GAT	CAT	AAC	AAT	TAT	AAT	GAA	GAT	AAT	ATT		966
345	Asn	Asp	Asn	Asp	Asp	Arg	Asp	His	Asn	Asn	Tyr	Asn	Glu	Asp	Asn	Ile	
346			295					300					305				
348	GGG	ATT	GAC	AAA	CAC	CAA	AAC	ATG	CAA	TAAATCTTG							1002
349	Gly	Ile	Asp	Lys	His	Gln	Asn	Met	Gln								

VERIFICATION SUMMARY

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TIME: 13:57:36

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L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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L:1302 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16, Value=[DNA]
L:1319 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17, Value=[DNA]
L:1336 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18, Value=[DNA]
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